



Supplementary Figure 1 Maximum likelihood (ML) phylogenetic trees of *Copia* and *Gypsy* LTR retrotransposon families. Sequences of intact (A) *Copia* and (B) *Gypsy* copies identified in *S. alba* and *S. caseolaris* were used for this analysis. Supporting values of each branch were calculated by resampling estimated log-likelihoods (RELL)-like local support values.